

OIPE

## RAW SEQUENCE LISTING

DATE: 06/20/2001

PATENT APPLICATION: US/09/873,409

TIME: 12:14:41

Input Set : A:\frank.ST25.txt

Output Set: N:\CRF3\06202001\I873409.raw

5 <110> APPLICANT: Frank, Markus  
 7 Sayegh, Mohamed  
 11 <120> TITLE OF INVENTION: A Gene Encoding a Multidrug Resistance Human P-Glycoprotein  
 12 Homologue on Chromosome 7p15-21 and Uses Thereof  
 16 <130> FILE REFERENCE: 81994/268611  
 C--> 20 <140> CURRENT APPLICATION NUMBER: US/09/873,409  
 C--> 20 <141> CURRENT FILING DATE: 2001-06-05  
 20 <160> NUMBER OF SEQ ID NOS: 19  
 24 <170> SOFTWARE: PatentIn version 3.0  
 28 <210> SEQ ID NO: 1  
 30 <211> LENGTH: 659  
 32 <212> TYPE: PRT  
 34 <213> ORGANISM: Homo sapiens  
 38 <400> SEQUENCE: 1  
 40 Met Leu Ala Glu Lys Gly Ala His Ala Glu Leu Met Ala Lys Arg Gly  
 41 1 5 10 15  
 43 Leu Tyr Tyr Ser Leu Val Met Ser Gln Asp Ile Lys Lys Ala Asp Glu  
 44 20 25 30  
 46 Gln Met Glu Ser Met Thr Tyr Ser Thr Glu Arg Lys Thr Asn Ser Leu  
 47 35 40 45  
 49 Pro Leu His Ser Val Lys Ser Ile Lys Ser Asp Phe Ile Asp Lys Ala  
 50 50 55 60  
 52 Glu Glu Ser Thr Gln Ser Lys Glu Ile Ser Leu Pro Glu Val Ser Leu  
 53 65 70 75 80  
 55 Leu Lys Ile Leu Lys Leu Asn Lys Pro Glu Trp Pro Phe Val Val Leu  
 56 85 90 95  
 58 Gly Thr Leu Ala Ser Val Leu Asn Gly Thr Val His Pro Val Phe Ser  
 59 100 105 110  
 61 Ile Ile Phe Ala Lys Ile Ile Thr Met Phe Gly Asn Asn Asp Lys Thr  
 62 115 120 125  
 64 Thr Leu Lys His Asp Ala Glu Ile Tyr Ser Met Ile Phe Val Ile Leu  
 65 130 135 140  
 67 Gly Val Ile Cys Phe Val Ser Tyr Phe Met Gln Gly Leu Phe Tyr Gly  
 68 145 150 155 160  
 70 Arg Ala Gly Glu Ile Leu Thr Met Arg Leu Arg His Leu Ala Phe Lys  
 71 165 170 175  
 73 Ala Met Leu Tyr Gln Asp Ile Ala Trp Phe Asp Glu Lys Glu Asn Ser  
 74 180 185 190  
 76 Thr Gly Gly Leu Thr Thr Ile Leu Ala Ile Asp Ile Ala Gln Ile Gln  
 77 195 200 205  
 79 Gly Ala Thr Gly Ser Arg Ile Gly Val Leu Thr Gln Asn Ala Thr Asn  
 80 210 215 220  
 82 Met Gly Leu Ser Val Ile Ile Ser Phe Ile Tyr Gly Trp Glu Met Thr  
 83 225 230 235 240  
 85 Phe Leu Ile Leu Ser Ile Ala Pro Val Leu Ala Val Thr Gly Met Ile  
 86 245 250 255  
 88 Glu Thr Ala Ala Met Thr Gly Phe Ala Asn Lys Asp Lys Gln Glu Leu

ENTERED

See p.5

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```

89          260          265          270
91 Lys His Ala Gly Lys Ile Ala Thr Glu Ala Leu Glu Asn Ile Arg Thr
92          275          280          285
94 Ile Val Ser Leu Thr Arg Glu Lys Ala Phe Glu Gln Met Tyr Glu Glu
95          290          295          300
97 Met Leu Gln Thr Gln His Arg Asn Thr Ser Lys Lys Ala Gln Ile Ile
98 305          310          315          320
100 Gly Ser Cys Tyr Ala Phe Ser His Ala Phe Ile Tyr Phe Ala Tyr Ala
101          325          330          335
103 Ala Gly Phe Arg Phe Gly Ala Tyr Leu Ile Gln Ala Gly Arg Met Thr
104          340          345          350
106 Pro Glu Gly Met Phe Ile Val Phe Thr Ala Ile Ala Tyr Gly Ala Met
107          355          360          365
109 Ala Ile Gly Lys Thr Leu Val Leu Ala Pro Glu Tyr Ser Lys Ala Lys
110          370          375          380
112 Ser Gly Ala Ala His Leu Phe Ala Leu Leu Glu Lys Lys Pro Asn Ile
113 385          390          395          400
115 Asp Ser Arg Ser Gln Glu Gly Lys Lys Pro Asp Thr Cys Glu Gly Asn
116          405          410          415
118 Leu Glu Phe Arg Glu Val Ser Phe Phe Tyr Pro Cys Arg Pro Asp Val
119          420          425          430
121 Phe Ile Leu Arg Gly Leu Ser Leu Ser Ile Glu Arg Gly Lys Thr Val
122          435          440          445
124 Ala Phe Val Gly Ser Ser Gly Cys Gly Lys Ser Thr Ser Val Gln Leu
125          450          455          460
127 Leu Gln Arg Leu Tyr Asp Pro Val Gln Gly Gln Val Leu Phe Asp Gly
128 465          470          475          480
130 Val Asp Ala Lys Glu Leu Asn Val Gln Trp Leu Arg Ser Gln Ile Ala
131          485          490          495
133 Ile Val Pro Gln Glu Pro Val Leu Phe Asn Cys Ser Ile Ala Glu Asn
134          500          505          510
136 Ile Ala Tyr Gly Asp Asn Ser Arg Val Val Pro Leu Asp Glu Ile Lys
137          515          520          525
139 Glu Ala Ala Asn Ala Ala Asn Ile His Ser Phe Ile Glu Gly Leu Pro
140          530          535          540
142 Glu Lys Tyr Asn Thr Gln Val Gly Leu Lys Gly Ala Gln Leu Ser Gly
143 545          550          555          560
145 Gly Gln Lys Gln Arg Leu Ala Ile Ala Arg Ala Leu Leu Gln Lys Pro
146          565          570          575
148 Lys Ile Leu Leu Leu Asp Glu Ala Thr Ser Ala Leu Asp Asn Asp Ser
149          580          585          590
151 Glu Lys Val Val Gln His Ala Leu Asp Lys Ala Arg Thr Gly Arg Thr
152          595          600          605
154 Cys Leu Val Val Thr His Arg Leu Ser Ala Ile Gln Asn Ala Asp Leu
155          610          615          620
157 Ile Val Val Leu His Asn Gly Lys Ile Lys Glu Gln Gly Thr His Gln
158 625          630          635          640
160 Glu Leu Leu Arg Asn Arg Asp Ile Tyr Phe Lys Leu Val Asn Ala Gln
161          645          650          655

```

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```

163 Ser Val Gln
166 <210> SEQ ID NO: 2
168 <211> LENGTH: 812
170 <212> TYPE: PRT
172 <213> ORGANISM: Homo sapiens
176 <400> SEQUENCE: 2
178 Met Val Asp Glu Asn Asp Ile Arg Ala Leu Asn Val Arg His Tyr Arg
179 1 5 10 15
181 Asp His Ile Gly Val Val Ser Gln Glu Pro Val Leu Phe Gly Thr Thr
182 20 25 30
184 Ile Ser Asn Asn Ile Lys Tyr Gly Arg Asp Asp Val Thr Asp Glu Glu
185 35 40 45
187 Met Glu Arg Ala Ala Arg Glu Ala Asn Ala Tyr Asp Phe Ile Met Glu
188 50 55 60
190 Phe Pro Asn Lys Phe Asn Thr Leu Val Gly Glu Lys Gly Ala Gln Met
191 65 70 75 80
193 Ser Gly Gly Gln Lys Gln Arg Ile Ala Ile Ala Arg Ala Leu Val Arg
194 85 90 95
196 Asn Pro Lys Ile Leu Ile Leu Asp Glu Ala Thr Ser Ala Leu Asp Ser
197 100 105 110
199 Glu Ser Lys Ser Ala Val Gln Ala Ala Leu Glu Lys Ala Ser Lys Gly
200 115 120 125
202 Arg Thr Thr Ile Val Val Ala His Arg Leu Ser Thr Ile Arg Ser Ala
203 130 135 140
205 Asp Leu Ile Val Thr Leu Lys Asp Gly Met Leu Ala Glu Lys Gly Ala
206 145 150 155 160
208 His Ala Glu Leu Met Ala Lys Arg Gly Leu Tyr Tyr Ser Leu Val Met
209 165 170 175
211 Ser Gln Asp Ile Lys Lys Ala Asp Glu Gln Met Glu Ser Met Thr Tyr
212 180 185 190
214 Ser Thr Glu Arg Lys Thr Asn Ser Leu Pro Leu His Ser Val Lys Ser
215 195 200 205
217 Ile Lys Ser Asp Phe Ile Asp Lys Ala Glu Glu Ser Thr Gln Ser Lys
218 210 215 220
220 Glu Ile Ser Leu Pro Glu Val Ser Leu Leu Lys Ile Leu Lys Leu Asn
221 225 230 235 240
223 Lys Pro Glu Trp Pro Phe Val Val Leu Gly Thr Leu Ala Ser Val Leu
224 245 250 255
226 Asn Gly Thr Val His Pro Val Phe Ser Ile Ile Phe Ala Lys Ile Ile
227 260 265 270
229 Thr Met Phe Gly Asn Asn Asp Lys Thr Thr Leu Lys His Asp Ala Glu
230 275 280 285
232 Ile Tyr Ser Met Ile Phe Val Ile Leu Gly Val Ile Cys Phe Val Ser
233 290 295 300
235 Tyr Phe Met Gln Gly Leu Phe Tyr Gly Arg Ala Gly Glu Ile Leu Thr
236 305 310 315 320
238 Met Arg Leu Arg His Leu Ala Phe Lys Ala Met Leu Tyr Gln Asp Ile
239 325 330 335
241 Ala Trp Phe Asp Glu Lys Glu Asn Ser Thr Gly Gly Leu Thr Thr Ile

```

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Input Set : A:\frank.ST25.txt

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```

242          340          345          350
244 Leu Ala Ile Asp Ile Ala Gln Ile Gln Gly Ala Thr Gly Ser Arg Ile
245          355          360          365
247 Gly Val Leu Thr Gln Asn Ala Thr Asn Met Gly Leu Ser Val Ile Ile
248          370          375          380
250 Ser Phe Ile Tyr Gly Trp Glu Met Thr Phe Leu Ile Leu Ser Ile Ala
251 385          390          395          400
253 Pro Val Leu Ala Val Thr Gly Met Ile Glu Thr Ala Ala Met Thr Gly
254          405          410          415
256 Phe Ala Asn Lys Asp Lys Gln Glu Leu Lys His Ala Gly Lys Ile Ala
257          420          425          430
259 Thr Glu Ala Leu Glu Asn Ile Arg Thr Ile Val Ser Leu Thr Arg Glu
260          435          440          445
262 Lys Ala Phe Glu Gln Met Tyr Glu Glu Met Leu Gln Thr Gln His Arg
263          450          455          460
265 Asn Thr Ser Lys Lys Ala Gln Ile Ile Gly Ser Cys Tyr Ala Phe Ser
266 465          470          475          480
268 His Ala Phe Ile Tyr Phe Ala Tyr Ala Ala Gly Phe Arg Phe Gly Ala
269          485          490          495
271 Tyr Leu Ile Gln Ala Gly Arg Met Thr Pro Glu Gly Met Phe Ile Val
272          500          505          510
274 Phe Thr Ala Ile Ala Tyr Gly Ala Met Ala Ile Gly Lys Thr Leu Val
275          515          520          525
277 Leu Ala Pro Glu Tyr Ser Lys Ala Lys Ser Gly Ala Ala His Leu Phe
278          530          535          540
280 Ala Leu Leu Glu Lys Lys Pro Asn Ile Asp Ser Arg Ser Gln Glu Gly
281 545          550          555          560
283 Lys Lys Pro Asp Thr Cys Glu Gly Asn Leu Glu Phe Arg Glu Val Ser
284          565          570          575
286 Phe Phe Tyr Pro Cys Arg Pro Asp Val Phe Ile Leu Arg Gly Leu Ser
287          580          585          590
289 Leu Ser Ile Glu Arg Gly Lys Thr Val Ala Phe Val Gly Ser Ser Gly
290          595          600          605
292 Cys Gly Lys Ser Thr Ser Val Gln Leu Leu Gln Arg Leu Tyr Asp Pro
293          610          615          620
295 Val Gln Gly Gln Val Leu Phe Asp Gly Val Asp Ala Lys Glu Leu Asn
296 625          630          635          640
298 Val Gln Trp Leu Arg Ser Gln Ile Ala Ile Val Pro Gln Glu Pro Val
299          645          650          655
301 Leu Phe Asn Cys Ser Ile Ala Glu Asn Ile Ala Tyr Gly Asp Asn Ser
302          660          665          670
304 Arg Val Val Pro Leu Asp Glu Ile Lys Glu Ala Ala Asn Ala Ala Asn
305          675          680          685
307 Ile His Ser Phe Ile Glu Gly Leu Pro Glu Lys Tyr Asn Thr Gln Val
308          690          695          700
310 Gly Leu Lys Gly Ala Gln Leu Ser Gly Gly Gln Lys Gln Arg Leu Ala
311 705          710          715          720
313 Ile Ala Arg Ala Leu Leu Gln Lys Pro Lys Ile Leu Leu Leu Asp Glu
314          725          730          735

```

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Input Set : A:\frank.ST25.txt

Output Set: N:\CRF3\06202001\I873409.raw

```

316 Ala Thr Ser Ala Leu Asp Asn Asp Ser Glu Lys Val Val Gln His Ala
317           740           745           750
319 Leu Asp Lys Ala Arg Thr Gly Arg Thr Cys Leu Val Val Thr His Arg
320           755           760           765
322 Leu Ser Ala Ile Gln Asn Ala Asp Leu Ile Val Val Leu His Asn Gly
323           770           775           780
325 Lys Ile Lys Glu Gln Gly Thr His Gln Glu Leu Leu Arg Asn Arg Asp
326 785           790           795           800
328 Ile Tyr Phe Lys Leu Val Asn Ala Gln Ser Val Gln
329           805           810

```

331 &lt;210&gt; SEQ ID NO: 3

333 &lt;211&gt; LENGTH: 131

335 &lt;212&gt; TYPE: PRT

337 &lt;213&gt; ORGANISM: Homo sapiens

341 &lt;400&gt; SEQUENCE: 3

```

343 Met Val Asp Glu Asn Asp Ile Arg Ala Leu Asn Val Arg His Tyr Arg
344 1           5           10           15
346 Asp His Ile Gly Val Val Ser Gln Glu Pro Val Leu Phe Gly Thr Thr
347           20           25           30
349 Ile Ser Asn Asn Ile Lys Tyr Gly Arg Asp Asp Val Thr Asp Glu Glu
350           35           40           45
352 Met Glu Arg Ala Ala Arg Glu Ala Asn Ala Tyr Asp Phe Ile Met Glu
353           50           55           60
355 Phe Pro Asn Lys Phe Asn Thr Leu Val Gly Glu Lys Gly Ala Gln Met
356 65           70           75           80
358 Ser Gly Gly Gln Lys Gln Arg Ile Ala Ile Ala Arg Ala Leu Val Arg
359           85           90           95
361 Asn Pro Lys Ile Leu Ile Leu Asp Glu Ala Thr Ser Ala Leu Asp Ser
362           100          105          110
364 Glu Ser Lys Ser Ala Val Gln Ala Ala Leu Glu Lys Asp Thr Pro Arg
365           115          120          125
367 Tyr Ser Phe
368           130

```

370 &lt;210&gt; SEQ ID NO: 4

372 &lt;211&gt; LENGTH: 1058

374 &lt;212&gt; TYPE: PRT

376 &lt;213&gt; ORGANISM: Homo sapiens

380 &lt;220&gt; FEATURE:

W--&gt; 382 &lt;221&gt; NAME/KEY: Note

384 &lt;222&gt; LOCATION: (66)..(66) ✓

386 &lt;223&gt; OTHER INFORMATION: Xaa at position 66 represents any L amino acid

392 &lt;400&gt; SEQUENCE: 4

```

394 Met Val Ile Ser Leu Thr Ser Lys Glu Leu Ser Ala Tyr Ser Lys Ala
395 1           5           10           15
397 Gly Ala Val Ala Glu Glu Val Leu Ser Ser Ile Arg Thr Val Ile Ala
398           20           25           30
400 Phe Arg Ala Gln Glu Lys Glu Leu Gln Arg Ser Phe Leu Leu Asn Ile
401           35           40           45
403 Thr Arg Tyr Ala Trp Phe Tyr Phe Pro Gln Trp Leu Leu Ser Cys Val

```

**Please Note:**

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

## VERIFICATION SUMMARY

PATENT APPLICATION: US/09/873,409

DATE: 06/20/2001

TIME: 12:14:42

Input Set : A:\frank.ST25.txt

Output Set: N:\CRF3\06202001\I873409.raw

L:20 M:270 C: Current Application Number differs, Replaced Current Application No  
L:20 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:382 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4  
L:406 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4  
L:607 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5  
L:661 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:1105 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:7  
L:1159 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7  
L:1584 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:12  
L:1601 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12  
L:1714 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:13  
L:1749 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13  
L:1996 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:15  
L:2031 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15